

containing nucleotide positions 6593-6595 of SEQ ID NO:7 were not sufficiently described in the specification.

Applicants respectfully traverse this rejection. Possession may be shown in many ways. For example, possession may be shown by describing an actual reduction to practice of the claimed invention. Possession may also be shown by a clear depiction of the invention in detailed drawings or in structural chemical formulas which permit a person skilled in the art to clearly recognize that applicant had possession of the claimed invention. An adequate written description of the invention may be shown by any description of sufficient, relevant, identifying characteristics so long as a person skilled in the art would recognize that the inventor had possession of the claimed invention. Moreover, what is conventional or well known to one of ordinary skill in the art need not be disclosed in detail. If a skilled artisan would have understood the inventor to be in possession of the claimed invention at the time of filing, even if every nuance of the claims is not explicitly described in the specification, then the adequate description requirement is met. MPEP §2163.

Claim 6 recites an isolated polynucleotide fragment of SEQ ID NO:7 comprising nucleotide positions 6593-6395 of SEQ ID NO: 7, wherein the fragment is at least 15 nucleotides in length. Applicants clearly disclosed the nucleotide sequence of SEQ ID NO:7 in the application as filed and state at page 3, lines 8-12, that the invention includes fragments of, *inter alia*, SEQ ID NO: 7 that are at least about 10 nucleotides in length. Clearly, Applicants were in possession of the complete nucleotide sequence of SEQ ID NO:7 at the time the application was filed, and thus must be said to have been in possession of portions of SEQ ID NO:7, particularly where Applicants clearly indicated at the cited pages that such fragments or portions were part of the invention.

Claim 8 recites a nucleic acid molecule that hybridizes under high stringency conditions to a nucleotide sequence comprising nucleotide positions 6593-6395 of SEQ ID NO: 7 and at least ten flanking nucleotides of SEQ ID NO:7 or the complement of said nucleotide sequence. Again, Applicants clearly disclosed the nucleotide sequence of SEQ ID NO: 7 and its complement in the Specification as filed. In addition, Applicants clearly describe in the Specification at page 17, line 11, through page 18, line 11, that the invention encompasses nucleic acid molecules that hybridize under high stringency conditions as set forth in the

application. The skilled artisan would know that the description of a particular nucleotide sequence (SEQ ID NO:7 or its complement) to which the claimed sequence hybridizes and the description of particular hybridization conditions are sufficient identifying characteristics to clearly indicate that Applicants were in possession of the claimed invention at the time the application was filed in accordance with MPEP §2163.

As shown by the comments above, one skilled in the art can reasonably conclude that the inventors had possession of the claimed invention at the time the application was filed. Therefore, reconsideration and withdrawal of the rejection are respectfully requested.

CONCLUSION

In view of the above amendments and remarks, it is believed that all claims are in condition for allowance, and it is respectfully requested that the application be passed to issue. If the Examiner feels that a telephone conference would expedite prosecution of this case, the Examiner is invited to call the undersigned at (978) 341-0036.

Respectfully submitted,

HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

By Lisa M. Treannie
Lisa M. Treannie
Registration No. 41,368
Telephone: (978) 341-0036
Facsimile: (978) 341-0136

Concord, MA 01742-9133

Dated: 7/8/03

MARKED UP VERSION OF AMENDMENTSSpecification Amendments Under 37 C.F.R. § 1.121(b)(1)(iii)

Replace the paragraph at page 42, lines 22 through 28 with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

Computational Analyses

World Wide Web-based hyper -text (http) sequence analysis included (using default parameters):

BLAST[: ncbi.nlm.nih.gov/cgi-bin/BLAST/nph-nesblast?Jform=1];

FASTA[: ebi.ac.uk/searches/fasta.html];

PSORT[: psort.nibb.ac.jp:8800];

EXPASY Proteomics tools[: expasy.ch/tools/];

BCM Search Launcher[: hgsc.bcm.tmc.edu/SearchLauncher/];

COILS (35) web server[: ch.embnnet.org/software/COILS_form.html];

and the [following] ftp site,[:] [mac-search-launcher\[: dot.bcm.tmc.edu/pub/software/search-launcher/\]](http://dot.bcm.tmc.edu/pub/software/search-launcher/).